

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

Oscar Johannes Maria GODDIJN  
Teunis Cornelis VERWOERD  
Ronny Wilhelmus Hermanus Henrika KRUTWAGEN  
Eline VOOGD

(ii) TITLE OF INVENTION:

ENHANCED ACCUMULATION OF TREHALOSE IN PLANTS

(iii) NUMBER OF SEQUENCES: 27

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LADAS & PARRY  
(B) STREET: 26 WEST 61 STREET  
(C) CITY: NEW YORK  
(D) STATE: NY  
(E) ZIP: 10023  
(F) COUNTRY: USA

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3-1/4" Disk 1.44 MB  
(B) COMPUTER: IBM PC Compatible  
(C) OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11  
(D) SOFTWARE: WordPerfect 6.1 for Windows

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/779,460  
(B) FILING DATE: 07-JAN-1997  
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PY000009/96

42070 03762280

27

(B) FILING DATE: 12-JAN-1996

(viii) : ATTORNEY/AGENT INFORMATION:

(A) NAME: MASS, Clifford J.

(B) REGISTRATION NO.: 30,086

(C) REF./DOCKET NO.: U-011098-6

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE NUMBER: (212) 708-1890

(B) TELEAX NUMBER: (212) - 246-8959

(C) TELEX NUMBER: 233288

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..2485

(D) OTHER INFORMATION: /function= "trehalose phosph.  
synthase and trehalose phosph. phosphatase"  
/product= "bipartite enzyme"

(ix) FEATURE:

(A) NAME/KEY: unsure

(B) LOCATION: 1609..1611

45070-034430

30

Parameter	1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2	
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TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 620 625 630	1923
CTG AGG CCG GTT ATG AAT CTT TAT ACA GAA ACT ACT GAC GGT TCG TAT Leu Arg Pro Val Met Asn Leu Tyr Thr Glu Thr Thr Asp Gly Ser Tyr 635 640 645	1971
ATT GAA AAG AAA GAA ACT GCA ATG GTT TGG CAC TAT GAA GAT GCT GAT Ile Glu Lys Lys Glu Thr Ala Met Val Trp His Tyr Glu Asp Ala Asp 650 655 660 665	2019
AAA GAT CTT GGG TTG GAG CAG GCT AAG GAA CTG TTG GAC CAT CTT GAA Lys Asp Leu Gly Leu Glu Gln Ala Lys Glu Leu Leu Asp His Leu Glu 670 675 680	2067
AAC GTG CTC GCT AAT GAG CCC GTT GGA GTG AAT CGA ACA GGT CAA TAC Asn Val Leu Ala Asn Glu Pro Val Gly Val Asn Arg Thr Gly Gln Tyr 685 690 695	2115
ATT GTA GAA GTT AAA CCA CAG TCC CCC ATT AAT TAC CTT CTT GTT ATG Ile Val Glu Val Lys Pro Gln Ser Pro Ile Asn Tyr Leu Leu Val Met 700 705 710	2163
ACA TTC ATA GGC ACT GAT TGT AGA ATC TTT AAC TTA AAT TTC TTT AAA Thr Phe Ile Gly Thr Asp Cys Arg Ile Phe Asn Leu Asn Phe Phe Lys 715 720 725	2211
TAT GAA TGC AAT TAT AGG GGG TCA CTA AAA GGT ATA GTT GCA GAG AAG Tyr Glu Cys Asn Tyr Arg Gly Ser Leu Lys Gly Ile Val Ala Glu Lys 730 735 740 745	2259
ATT TTT GCG TTC ATG GCT AAA AAG GGA AAA CAG GCT GAT TTC GTG TTG Ile Phe Ala Phe Met Ala Lys Lys Gly Lys Gln Ala Asp Phe Val Leu 750 755 760	2307
ACG TTG AAT GAT AGA AGT GAT GAA GAC ATG TTT GTG GCC ATT GGG GAT Thr Leu Asn Asp Arg Ser Asp Glu Asp Met Phe Val Ala Ile Gly Asp 765 770 775	2355
GGA ATA AAA AAG GGT CGG ATA ACT AAC AAC AAT TCA GTG TTT ACA TGC Gly Ile Lys Lys Gly Arg Ile Thr Asn Asn Asn Ser Val Phe Thr Cys 780 785 790	2403
GTA GTG GGA GAG AAA CCG AGT GCA GCT GAG TAC TTT TTA AAT GAT GTC Val Val Gly Glu Lys Pro Ser Ala Ala Glu Tyr Phe Leu Asn Asp Val 795 800 805	2451
TCG AGA AGC TCC GGG TGT CTC AGC AAC CAA GGA T GATCCGGAAG Ser Arg Ser Ser Gly Cys Leu Ser Asn Gln Gly 810 815 820	2495
CTTCTCGTGA TCTTTATGAG TTAAAAGTTT TCGACTTTTT CTTCATCAAG ATTCATGGGA	2555

AAGTTGTTCA ATATGAACTT GTGTTCTTGG TTCTGGATTT TAGGGAGTCT ATGGATATAA

2615

CATTTC

2621

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ile Leu Leu His Leu Met Pro Leu Gln Met Leu Pro Asn Arg Leu  
1 5 10 15  
Ile Val Val Ser Asn Gln Leu Pro Ile Ile Ala Arg Leu Arg Leu Thr  
20 25 30  
Thr Met Glu Gly Pro Phe Gly Ile Ser Leu Gly Thr Arg Val Arg Phe  
35 40 45  
Thr Cys Thr Ser Lys Met His Tyr Pro Gln Pro Leu Arg Phe Ser Ile  
50 55 60  
Leu Gly Asp Pro Leu Arg Ala Asp Val Gly Pro Thr Glu Gln Asp Asp  
65 70 75 80  
Val Ser Lys Thr Leu Leu Asp Arg Phe Asn Cys Val Ala Val Phe Val  
85 90 95  
Pro Thr Ser Lys Trp Asp Gln Tyr Tyr His Cys Phe Cys Lys Gln Tyr  
100 105 110  
Leu Trp Pro Ile Phe His Tyr Lys Val Pro Ala Ser Asp Val Lys Ser  
115 120 125  
Val Pro Asn Ser Arg Asp Ser Trp Asn Ala Tyr Val His Val Asn Lys  
130 135 140  
Glu Phe Ser Gln Lys Val Met Glu Ala Val Thr Asn Arg Ser Asn Tyr  
145 150 155 160  
Val Trp Ile His Asp Tyr His Leu Met Thr Leu Pro Thr Phe Leu Arg  
165 170 175  
Arg Asp Phe Cys Arg Phe Lys Ile Gly Phe Phe Leu His Ser Pro Phe  
180 185 190  
Pro Ser Ser Glu Val Tyr Lys Thr Leu Pro Met Arg Asn Glu Leu Leu  
195 200 205

Lys	Gly	Leu	Leu	Asn	Ala	Asp	Leu	Ile	Gly	Phe	His	Thr	Tyr	Asp	Tyr
210						215						220			
Ala	Arg	His	Phe	Leu	Thr	Cys	Cys	Ser	Arg	Met	Phe	Gly	Leu	Asp	His
225					230					235					240
Gln	Leu	Lys	Arg	Gly	Tyr	Ile	Phe	Leu	Glu	Tyr	Asn	Gly	Arg	Ser	Ile
				245					250					255	
Glu	Ile	Lys	Ile	Lys	Ala	Ser	Gly	Ile	His	Val	Gly	Arg	Met	Glu	Ser
			260					265					270		
Tyr	Leu	Ser	Gln	Pro	Asp	Thr	Arg	Leu	Gln	Val	Gln	Glu	Val	Gln	Lys
		275					280					285			
Arg	Ser	Lys	Glu	Ile	Val	Leu	Leu	Gly	Val	Asp	Asp	Leu	Asp	Ile	Phe
	290					295					300				
Lys	Gly	Val	Asn	Phe	Lys	Val	Leu	Ala	Leu	Glu	Lys	Leu	Leu	Lys	Ser
305					310					315					320
His	Pro	Ser	Trp	Gln	Gly	Arg	Val	Glu	Lys	Val	Gln	Ile	Leu	Asn	Pro
				325					330					335	
Leu	Arg	Arg	Cys	Gln	Asp	Val	Asp	Glu	Ile	Asn	Ala	Glu	Ile	Arg	Thr
			340					345					350		
Val	Cys	Glu	Arg	Ile	Asn	Asn	Glu	Leu	Gly	Ser	Pro	Gly	Tyr	Gln	Pro
		355					360					365			
Val	Val	Leu	Ile	Asp	Gly	Pro	Val	Ser	Leu	Ser	Glu	Lys	Ala	Ala	Tyr
	370					375					380				
Tyr	Ala	Ile	Ala	Asp	Met	Ala	Ile	Val	Thr	Pro	Leu	Arg	Asp	Gly	Leu
385				390						395					400
Asn	Leu	Ile	Pro	Tyr	Glu	Tyr	Val	Val	Ser	Arg	Gln	Ser	Val	Asn	Asp
				405					410					415	
Pro	Asn	Pro	Asn	Thr	Pro	Lys	Lys	Ser	Met	Leu	Val	Val	Ser	Glu	Phe
			420					425					430		
Ile	Gly	Val	Ser	Leu	Ser	Leu	Thr	Gly	Ala	Ile	Arg	Val	Asn	Pro	Trp
		435					440					445			
Asp	Glu	Leu	Glu	Thr	Ala	Glu	Ala	Leu	Tyr	Asp	Ala	Leu	Met	Ala	Pro
	450					455					460				
Asp	Asp	His	Lys	Glu	Thr	Ala	His	Met	Lys	Gln	Tyr	Gln	Tyr	Ile	Ile
465					470					475					480
Ser	His	Asp	Val	Ala	Asn	Trp	Ala	Ser	Phe	Phe	Gln	Asp	Leu	Glu	Gln
				485					490					495	



Ala	Cys	Ile	Asp	His	Ser	Arg	Lys	Arg	Cys	Met	Asn	Leu	Gly	Phe	Gly
			500						505			510			
Leu	Asp	Thr	Arg	Val	Val	Phe	Leu	Met	Arg	Ser	Leu	Ala	Ser	Trp	Ile
			515						520			525			
Lys	Met	Ser	Trp	Lys	Asn	Ala	Tyr	Ser	Met	Ala	Gln	Asn	Arg	Ala	Ile
			530			535			540						
Leu	Leu	Asp	Tyr	Asp	Gly	Thr	Val	Thr	Pro	Ser	Ile	Ser	Lys	Ser	Pro
545			550						555			560			
Thr	Glu	Ala	Val	Ile	Ser	Met	Ile	Asn	Lys	Leu	Cys	Asn	Asp	Pro	Lys
			565						570			575			
Asn	Met	Val	Phe	Ile	Val	Ser	Gly	Arg	Ser	Arg	Glu	Lys	Ile	Leu	Ala
			580			585						590			
Val	Gly	Ser	Ala	Arg	Val	Arg	Thr	Arg	His	Cys	Thr	Glu	His	Gly	Tyr
			595			600						605			
Phe	Ile	Arg	Trp	Ala	Gly	Asp	Gln	Glu	Trp	Glu	Thr	Cys	Ala	Arg	Glu
610			615						620						
Asn	Asn	Val	Gly	Trp	Met	Asp	Gly	Asn	Leu	Arg	Pro	Val	Met	Asn	Leu
625			630						635			640			
Tyr	Thr	Glu	Thr	Thr	Asp	Gly	Ser	Tyr	Ile	Glu	Lys	Lys	Glu	Thr	Ala
			645						650			655			
Met	Val	Trp	His	Tyr	Glu	Asp	Ala	Asp	Lys	Asp	Leu	Gly	Leu	Glu	Gln
			660			665						670			
Ala	Lys	Glu	Leu	Leu	Asp	His	Leu	Glu	Asn	Val	Leu	Ala	Asn	Glu	Pro
675						680						685			
Val	Gly	Val	Asn	Arg	Thr	Gly	Gln	Tyr	Ile	Val	Glu	Val	Lys	Pro	Gln
690			695						700						
Ser	Pro	Ile	Asn	Tyr	Leu	Leu	Val	Met	Thr	Phe	Ile	Gly	Thr	Asp	Cys
705			710						715			720			
Arg	Ile	Phe	Asn	Leu	Asn	Phe	Phe	Lys	Tyr	Glu	Cys	Asn	Tyr	Arg	Gly
			725						730			735			
Ser	Leu	Lys	Gly	Ile	Val	Ala	Glu	Lys	Ile	Phe	Ala	Phe	Met	Ala	Lys
			740			745						750			
Lys	Gly	Lys	Gln	Ala	Asp	Phe	Val	Leu	Thr	Leu	Asn	Asp	Arg	Ser	Asp
755						760						765			
Glu	Asp	Met	Phe	Val	Ala	Ile	Gly	Asp	Gly	Ile	Lys	Lys	Gly	Arg	Ile
770			775						780						

Thr Asn Asn Asn Ser Val Phe Thr Cys Val Val Gly Glu Lys Pro Ser  
785 790 795 800

Ala Ala Glu Tyr Phe Leu Asn Asp Val Ser Arg Ser Ser Gly Cys Leu  
805 810 815

Ser Asn Gln Gly  
820

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGCTTATGT TGCCATATAG AGTAG

25

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTAGTTGCCA TGGTGCAAAT GTTC

24

38

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGCTCTGCAG TGAGGTACCA

20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GACGTCCTC CATGGTTCGA

20

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTACCCTGCA GTGTGACCCT AGAC

24

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGATTCATA GAAGCTTAGA T

21

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: Kardal

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 161..1906

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 842..850
- (D) OTHER INFORMATION: /function= "putative glycosylationsite"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTTTTCTGAG TAATAACATA GGCATTGATT TTTTTCAT TAATAACACC TGCAAACATT 60

CCCATTGCCG GCATTCTCTG TTCTTACAAA AAAAAACATT TTTTGTTC CATAAATTAG 120

254070-09462280

TTATGGCATC AGTATTGAAC CCTTTAACTT GTTATACAAT ATG GGT AAA GCT ATA	175
Met Gly Lys Ala Ile	
1 5	
ATT TTT ATG ATT TTT ACT ATG TCT ATG AAT ATG ATT AAA GCT GAA ACT	223
Ile Phe Met Ile Phe Thr Met Ser Met Asn Met Ile Lys Ala Glu Thr	
10 15 20	
TGC AAA TCC ATT GAT AAG GGT CCT GTA ATC CCA ACA ACC CCT TTA GTG	271
Cys Lys Ser Ile Asp Lys Gly Pro Val Ile Pro Thr Thr Pro Leu Val	
25 30 35	
ATT TTT CTT GAA AAA GTT CAA GAA GCT GCT CTT CAA ACT TAT GGC CAT	319
Ile Phe Leu Glu Lys Val Gln Glu Ala Ala Leu Gln Thr Tyr Gly His	
40 45 50	
AAA GGG TTT GAT GCT AAA CTG TTT GTT GAT ATG TCA CTG AGA GAG AGT	367
Lys Gly Phe Asp Ala Lys Leu Phe Val Asp Met Ser Leu Arg Glu Ser	
55 60 65	
CTT TCA GAA ACA GTT GAA GCT TTT AAT AAG CTT CCA AGA GTT GTG AAT	415
Leu Ser Glu Thr Val Glu Ala Phe Asn Lys Leu Pro Arg Val Val Asn	
70 75 80 85	
GGT TCA ATA TCA AAA AGT GAT TTG GAT GGT TTT ATA GGT AGT TAC TTG	463
Gly Ser Ile Ser Lys Ser Asp Leu Asp Gly Phe Ile Gly Ser Tyr Leu	
90 95 100	
AGT AGT CCT GAT AAG GAT TTG GTT TAT GTT GAG CCT ATG GAT TTT GTG	511
Ser Ser Pro Asp Lys Asp Leu Val Tyr Val Glu Pro Met Asp Phe Val	
105 110 115	
GCT GAG CCT GAA GGC TTT TTG CCA AAG GTG AAG AAT TCT GAG GTG AGG	559
Ala Glu Pro Glu Gly Phe Leu Pro Lys Val Lys Asn Ser Glu Val Arg	
120 125 130	
GCA TGG GCA TTG GAG GTG CAT TCA CTT TGG AAG AAT TTA AGT AGG AAA	607
Ala Trp Ala Leu Glu Val His Ser Leu Trp Lys Asn Leu Ser Arg Lys	
135 140 145	
GTG GCT GAT CAT GTA TTG GAA AAA CCA GAG TTG TAT ACT TTG CTT CCA	655
Val Ala Asp His Val Leu Glu Lys Pro Glu Leu Tyr Thr Leu Leu Pro	
150 155 160 165	
TTG AAA AAT CCA GTT ATT ATA CCG GGA TCG CGT TTT AAG GAG GTT TAT	703
Leu Lys Asn Pro Val Ile Ile Pro Gly Ser Arg Phe Lys Glu Val Tyr	
170 175 180	
TAT TGG GAT TCT TAT TGG GTA ATA AGG GGT TTG TTA GCA AGC AAA ATG	751
Tyr Trp Asp Ser Tyr Trp Val Ile Arg Gly Leu Leu Ala Ser Lys Met	
185 190 195	

TAT GAA ACT GCA AAA GGG ATT GTG ACT AAT CTG GTT TCT CTG ATA GAT	799
Tyr Glu Thr Ala Lys Gly Ile Val Thr Asn Leu Val Ser Leu Ile Asp	
200 205 210	
CAA TTT GGT TAT GTT CTT AAC GGT GCA AGA GCA TAC TAC AGT AAC AGA	847
Gln Phe Gly Tyr Val Leu Asn Gly Ala Arg Ala Tyr Tyr Ser Asn Arg	
215 220 225	
AGT CAG CCT CCT GTC CTG GCC ACG ATG ATT GTT GAC ATA TTC AAT CAG	895
Ser Gln Pro Pro Val Leu Ala Thr Met Ile Val Asp Ile Phe Asn Gln	
230 235 240 245	
ACA GGT GAT TTA AAT TTG GTT AGA AGA TCC CTT CCT GCT TTG CTC AAG	943
Thr Gly Asp Leu Asn Leu Val Arg Arg Ser Leu Pro Ala Leu Leu Lys	
250 255 260	
GAG AAT CAT TTT TGG AAT TCA GGA ATA CAT AAG GTG ACT ATT CAA GAT	991
Glu Asn His Phe Trp Asn Ser Gly Ile His Lys Val Thr Ile Gln Asp	
265 270 275	
GCT CAG GGA TCA AAC CAC AGC TTG AGT CGG TAC TAT GCT ATG TGG AAT	1039
Ala Gln Gly Ser Asn His Ser Leu Ser Arg Tyr Tyr Ala Met Trp Asn	
280 285 290	
AAG CCC CGT CCA GAA TCG TCA ACT ATA GAC AGT GAA ACA GCT TCC GTA	1087
Lys Pro Arg Pro Glu Ser Ser Thr Ile Asp Ser Glu Thr Ala Ser Val	
295 300 305	
CTC CCA AAT ATA TGT GAA AAA AGA GAA TTA TAC CGT GAA CTG GCA TCA	1135
Leu Pro Asn Ile Cys Glu Lys Arg Glu Leu Tyr Arg Glu Leu Ala Ser	
310 315 320 325	
GCT GCT GAA AGT GGA TGG GAT TTC AGT TCA AGA TGG ATG AGC AAC GGA	1183
Ala Ala Glu Ser Gly Trp Asp Phe Ser Ser Arg Trp Met Ser Asn Gly	
330 335 340	
TCT GAT CTG ACA ACA ACT AGT ACA ACA TCA ATT CTA CCA GTT GAT TTG	1231
Ser Asp Leu Thr Thr Thr Ser Thr Thr Ser Ile Leu Pro Val Asp Leu	
345 350 355	
AAT GCA TTC CTT CTG AAG ATG GAA CTT GAC ATT GCC TTT CTA GCA AAT	1279
Asn Ala Phe Leu Leu Lys Met Glu Leu Asp Ile Ala Phe Leu Ala Asn	
360 365 370	
CTT GTT GGA GAA AGT AGC ACG GCT TCA CAT TTT ACA GAA GCT GCT CAA	1327
Leu Val Gly Glu Ser Ser Thr Ala Ser His Phe Thr Glu Ala Ala Gln	
375 380 385	
AAT AGA CAG AAG GCT ATA AAC TGT ATC TTT TGG AAC GCA GAG ATG GGG	1375
Asn Arg Gln Lys Ala Ile Asn Cys Ile Phe Trp Asn Ala Glu Met Gly	
390 395 400 405	

CAA TGG CTT GAT TAC TGG CTT ACC AAC AGC GAC ACA TCT GAG GAT ATT	1423
Gln Trp Leu Asp Tyr Trp Leu Thr Asn Ser Asp Thr Ser Glu Asp Ile	
410 415 420	
TAT AAA TGG GAA GAT TTG CAC CAG AAC AAG AAG TCA TTT GCC TCT AAT	1471
Tyr Lys Trp Glu Asp Leu His Gln Asn Lys Lys Ser Phe Ala Ser Asn	
425 430 435	
TTT GTT CCG CTG TGG ACT GAA ATT TCT TGT TCA GAT AAT AAT ATC ACA	1519
Phe Val Pro Leu Trp Thr Glu Ile Ser Cys Ser Asp Asn Asn Ile Thr	
440 445 450	
ACT CAG AAA GTA GTT CAA AGT CTC ATG AGC TCG GGC TTG CTT CAG CCT	1567
Thr Gln Lys Val Val Gln Ser Leu Met Ser Ser Gly Leu Leu Gln Pro	
455 460 465	
GCA GGG ATT GCA ATG ACC TTG TCT AAT ACT GGA CAG CAA TGG GAT TTT	1615
Ala Gly Ile Ala Met Thr Leu Ser Asn Thr Gly Gln Gln Trp Asp Phe	
470 475 480 485	
CCG AAT GGT TGG CCC CCC CTT CAA CAC ATA ATC ATT GAA GGT CTC TTA	1663
Pro Asn Gly Trp Pro Pro Leu Gln His Ile Ile Ile Glu Gly Leu Leu	
490 495 500	
AGG TCT GGA CTA GAA GAG GCA AGA ACC TTA GCA AAA GAC ATT GCT ATT	1711
Arg Ser Gly Leu Glu Glu Ala Arg Thr Leu Ala Lys Asp Ile Ala Ile	
505 510 515	
CGC TGG TTA AGA ACT AAC TAT GTG ACT TAC AAG AAA ACC GGT GCT ATG	1759
Arg Trp Leu Arg Thr Asn Tyr Val Thr Tyr Lys Lys Thr Gly Ala Met	
520 525 530	
TAT GAA AAA TAT GAT GTC ACA AAA TGT GGA GCA TAT GGA GGT GGT GGT	1807
Tyr Glu Lys Tyr Asp Val Thr Lys Cys Gly Ala Tyr Gly Gly Gly Gly	
535 540 545	
GAA TAT ATG TCC CAA ACG GGT TTC GGA TGG TCA AAT GGC GTT GTA CTG	1855
Glu Tyr Met Ser Gln Thr Gly Phe Gly Trp Ser Asn Gly Val Val Leu	
550 555 560 565	
GCA CTT CTA GAG GAA TTT GGA TGG CCT GAA GAT TTG AAG ATT GAT TGC	1903
Ala Leu Leu Glu Glu Phe Gly Trp Pro Glu Asp Leu Lys Ile Asp Cys	
570 575 580	
TAATGAGCAA GTAGAAAAGC CAAATGAAAC ATCATTGAGT TTTATTTTCT TCTTTTGTTA	1963
AAATAAGCTG CAATGGTTTG CTGATAGTTT ATGTTTGTGTA TTACTATTTC ATAAGGTTTT	2023
TGTACCATAT CAAGTGATAT TACCATGAAC TATGTCGTTT GGACTCTTCA AATCGGATTT	2083
TGCAAAAATA ATGCAGTTTT GGAGAATCCG ATAACATAGA CCATGTATGG ATCTAAATTG	2143
TAAACAGCTT ACTATATTAA GTAAAAGAAA GATGATTCCT CTGCTTTAAA AAAAAAAAAA	2203

262010-09462280

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

Met Gly Lys Ala Ile Ile Phe Met Ile Phe Thr Met Ser Met Asn Met
 1             5             10             15

Ile Lys Ala Glu Thr Cys Lys Ser Ile Asp Lys Gly Pro Val Ile Pro
      20             25             30

Thr Thr Pro Leu Val Ile Phe Leu Glu Lys Val Gln Glu Ala Ala Leu
      35             40             45

Gln Thr Tyr Gly His Lys Gly Phe Asp Ala Lys Leu Phe Val Asp Met
      50             55             60

Ser Leu Arg Glu Ser Leu Ser Glu Thr Val Glu Ala Phe Asn Lys Leu
      65             70             75             80

Pro Arg Val Val Asn Gly Ser Ile Ser Lys Ser Asp Leu Asp Gly Phe
      85             90             95

Ile Gly Ser Tyr Leu Ser Ser Pro Asp Lys Asp Leu Val Tyr Val Glu
      100            105            110

Pro Met Asp Phe Val Ala Glu Pro Glu Gly Phe Leu Pro Lys Val Lys
      115            120            125

Asn Ser Glu Val Arg Ala Trp Ala Leu Glu Val His Ser Leu Trp Lys
      130            135            140

Asn Leu Ser Arg Lys Val Ala Asp His Val Leu Glu Lys Pro Glu Leu
      145            150            155            160

Tyr Thr Leu Leu Pro Leu Lys Asn Pro Val Ile Ile Pro Gly Ser Arg
      165            170            175

Phe Lys Glu Val Tyr Tyr Trp Asp Ser Tyr Trp Val Ile Arg Gly Leu
      180            185            190

Leu Ala Ser Lys Met Tyr Glu Thr Ala Lys Gly Ile Val Thr Asn Leu
      195            200            205

```

09779460-04097





Ile Glu Gly Leu Leu Arg Ser Gly Leu Glu Glu Ala Arg Thr Leu Ala  
500 505 510

Lys Asp Ile Ala Ile Arg Trp Leu Arg Thr Asn Tyr Val Thr Tyr Lys  
515 520 525

Lys Thr Gly Ala Met Tyr Glu Lys Tyr Asp Val Thr Lys Cys Gly Ala  
530 535 540

Tyr Gly Gly Gly Gly Glu Tyr Met Ser Gln Thr Gly Phe Gly Trp Ser  
545 550 555 560

Asn Gly Val Val Leu Ala Leu Leu Glu Glu Phe Gly Trp Pro Glu Asp  
565 570 575

Leu Lys Ile Asp Cys  
580

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGYGGNMGMT TYRWNGARKT MTAYKRYTGG GAC

33

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

46

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTNCCNGGNG GNCGNTTYRW NGARKT

26

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- 41
- (A) NAME/KEY: modified\_base
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGNGGYTGNS WNCGNRYRNAG RTARTA

26

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /mod\_base= i

Figure 1 consists of 12 scatter plots, labeled (a) through (l), arranged in a 6x2 grid. Each plot shows the relationship between the 'Number of children' (x-axis, ranging from 0 to 10) and a specific variable (y-axis). The variables are: (a) Age of mother, (b) Age of father, (c) Age of first child, (d) Age of last child, (e) Age of youngest child, (f) Age of oldest child, (g) Age of child at birth, (h) Age of child at death, (i) Age of child at marriage, (j) Age of child at divorce, (k) Age of child at remarriage, and (l) Age of child at remarriage. In all plots, there is a clear positive linear trend, indicating that as the number of children increases, the value of the variable on the y-axis also increases. The y-axis scales vary between plots, reflecting the different ranges of the variables.

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47  
(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCATCCTAAT ACGACTCACT ATAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CACAACAGGC TGGTATCCCG

20

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAATAACGAA CTGGGAAGCC

20

CCATCCTAAT ACGACTCACT ATAGGGC

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACTCACTATA GGGCTCGAGC GGC

23

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAYNTNATNT GGRTNCAYGA YTAYCA

26

262070-03462280

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCNACNGTRC ANGCRAANAC

20

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO



(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 2  
 (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 14  
 (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TNGGNTKN TT YYTNCAYAYN CCNTTYCC

28

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /mod\_base= i

[illegible]

- (ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

20

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(A) NAME/KEY: modified\_base  
(B) LOCATION: 9  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified\_base  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified\_base  
(B) LOCATION: 15  
(D) OTHER INFORMATION: /mod base= i

(A) NAME/KEY: modified\_base  
(B) LOCATION: 18  
(D) OTHER INFORMATION: /mod base= i

20

25

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /mod\_base= i

- (ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 17  
 (D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TCRTCNGTRA ARTCRTCNCC

20

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /mod\_base= i

- (ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /mod\_base= i

- (ix) FEATURE:  
 (A) NAME/KEY: modified\_base  
 (B) LOCATION: 15

0577940-0409

(D) OTHER INFORMATION: /mod\_base= i

(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: 21

(D) OTHER INFORMATION: /mod\_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GYNACNARRT TCATNCCRTC NC

22

09779460 040797